

SEA ID NO: 2

661 QGSGAAGPRLFTIHLIDANTDLNRKAHTCFNRIDIPPYESYKLYEKLTAVEETCGFA 720

722 VE 723

721 VE 722

JLT 4

13384

AAW13384 standard; protein; 748 AA.

AAW13384;

10-JUL-1997 (first entry)

Human protein ubiquitin ligase pub1.

Protein ubiquitin ligase; pub1; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.

Homo sapiens.

WO9712962-A1.

10-APR-1997.

04-OCT-1996; 96WO-US015930.

04-OCT-1995; 95US-00539205.

(COLD-) COLD SPRING HARBOR LAB.

Beach D, Caligiuri M, Nefsky B;

WPI; 1997-226206/20.

N-PSDB; AAT47040.

Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved in cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and proliferation.

Claim 1; Page 74-77; 109pp; English.

Human protein ubiquitin ligases pub1 (AAW13384), pub2 (AAW13385) and pub3 (AAW13386) are homologues of fission yeast pub1 (AAW13387) and were identified from cDNA clones (AAT47040-42) obt'd. e.g. from a keratinocyte cDNA library. Pub polypeptides can be produced in transfected host cells. They can control the steady state level of cdc25 phosphatase, the degree of CDK kinase (e.g. cdc2) dephosphorylation and the steady state level of p53 (controlling the degree of cell cycle regulation of p53). They can regulate cell or tissue differentiation, or cell growth or proliferation by affecting other proteins, can be a specific (ant)agonist of wild-type protein function and may be used as immunogens to elicit a specific immune residue

Sequence 748 AA;

Query Match 77.3%; Score 3001; DB 2; Length 748;

Best Local Similarity 74.6%; Pred. No. 1.5e-285;

Matches 565; Conservative 63; Mismatches 71; Indels 58; Gaps 8;

QY 5 IKRLTVLCARNLAKKDFPRLDPFPAKIVDGGGCHSTDTVKNLDPKNNQHYDLVIGK 64

DB 12 VKRLTVLCARNLVKKDFPRLDPFPAKIVDGGGCHSTDTVKNLDPKNNQHYDLVIGK 71

QY 65 TDSITISVWVHKKIKKQAGFGVRLLSNAISRLKDTGVRDLCKLNPSTDVAVRGQ 124

DB 72 SDSVTISVWVHKKIKKQAGFGVRLLSNAISRLKDTGVRDLCKLNPSTDVAVRGQ 131

QY 125 IVVSLQTRDRIGTGGVVDCCGELLE-----GTVY----- 155

DB 132 IVVSLQSRDRIGTGGVVDCCGELLE-----GTVY----- 191

QY 156 --EDSGPGRPLSCFMBEPAPYDSTGAAAGGNCRFVESPQORLOAQELRNPVGRSL 213

DB 192 ASEYSPGRPLSCFVDENTPISGTNGATCG-----OSSPRLAERVRQRNRNTM 242

QY 214 QTPONRPHGOSPELPEGYEORTTVOGQVYFLHTQTGVTWHDPRIPRDLNSVNCDELGP 273

DB 243 ---SRKTLHTPDLPEGYEORTTVOGQVYFLHTQTGVTWHDPRIPRDLNSVNCDELGP 298

QY 274 LPPGWEVSTVSGRIYFYVDHNNRTTQFTDPR---LHHIMHQCQLKPEQPPLPSEGS 329

DB 299 LPPGWEIRNTATGRVYFVDHNNRTTQFTDPRLSANLHLVLRNQQLADQOQQQVW----S 354

QY 330 L---EDELPAQRYERDLVQKLKVLRLHLSLQQAQCHRIEVSREIPEESTRQIMQNR 386

DB 355 LCPDDTECLTVPRYKRDVLVQKLKILRQLSQOQFQAGHCRIEVSREIPEESTRQIMQNR 414

QY 387 PKDLKRLMVKPRGEGGLDYGVAREWLYLLCHEMLNPFYGLFOYSTDNIMYQLINPDSS 446

DB 415 PKDLKRLMVKPRGEGGLDYGVAREWLYLLCHEMLNPFYGLFOYSTDNIMYQLINPDSS 474

QY 447 INPDHLSYFHFVGRIMGLAVFHGHVINGGFTVPFPYKOLLGKPIOLSLESVDLPHKSLV 506

DB 475 VNPHELVSFHFVGRIMGLAVFHGHVINGGFTVPFPYKOLLGKPIOLSLESVDLPHKSLV 534

QY 507 WILENDITPVLDTHTFCVEHNAFGRILQHELKPNRNPVTEENKKEYVRLYVNRVFRGI 566

DB 535 WILENDITPVLDTHTFCVEHNAFGRILQHELKPNRNPVTEENKKEYVRLYVNRVFRGI 594

QY 567 EAOFLALQGFNHLIPOHLLKPFDOKELELLIIGLDKLDLNDKSNTRLKHCVADSNVR 626

DB 595 EAOFLALQGFNHLIPOHLLKPFDOKELELLIIGLDKLDLNDKSNTRLKHCVADSNVR 654

QY 627 WFWOAVETDEERRARLLQFVTGSTRVPLQGFKAQSGSTGAAGPRLFTIHLIDANTDNL 686

DB 655 WFWOAVETDEERRARLLQFVTGSTRVPLQGFKAQSGSTGAAGPRLFTIHLIDANTDNL 711

QY 687 KAHTCFNRIDIPPYESYKLYEKLTAVEETCGFAVE 723

DB 712 KAHTCFNRIDIPPYESYKLYEKLTAVEETCGFAVE 748

RESULT 5

AAB31477

ID AAB31477 standard; protein; 748 AA.

XX AAB31477;

AC AAB31477;

DT 20-APR-2001 (first entry)

XX Amino acid sequence of a human Smurf2 polypeptide.

DE Smurf1; Smurf2; Smad signal transduction; bone morphogenic protein; BMP;

KW transforming growth factor-beta; human; TGF-beta; chondrogenesis;

KW osteogenesis; blood differentiation; cartilage formation; hair growth;

KW neural tube patterning; retinal development; heart induction;

KW morphogenesis; tooth formation; gamete formation.

XX Homo sapiens.

OS WO200077168-A2.

PN 21-DEC-2000.

XX 12-JUN-2000; 2000WO-US016250.

PD 11-JUN-1999; 99US-0138969P.

XX (UTNY) UNIV NEW YORK STATE RES FOUND.

PA (HSCR-) HSC RES & DEV LP.

XX Thomsen GH, Wrana J;

PI WPI; 2001-071267/08.

DB

applicant

development, heart induction and morphogenesis, hair growth, tooth formation, gamete formation and a wide variety of tissue and organ formation processes, and hinder the regeneration, growth, maintenance, etc., of bone and other tissues that are dependent on the BMP pathway. The polypeptide is useful for screening for various drugs and/or antibodies that can either enhance the BMP pathway, or inhibit it

XX SQ Sequence 748 AA;

Query Match 100.0%; Score 4038; DB 4; Length 748;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 748; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNPGRRNGPVKRLTLVLCANLVKDDFFRLPDPFAKVVVDGSGQCHSTDTVKNTLDPK 60
 DB 1 MSNPGRRNGPVKRLTLVLCANLVKDDFFRLPDPFAKVVVDGSGQCHSTDTVKNTLDPK 60

QY 61 WNOHYDLYIGKSDSVTISVWVNHKKIHKQAGFLGCVRLLSNAINRLKDTGYQRLDLCKL 120
 DB 61 WNOHYDLYIGKSDSVTISVWVNHKKIHKQAGFLGCVRLLSNAINRLKDTGYQRLDLCKL 120

QY 121 GENDNDTVRGQVWSLQSRDRIGTGQVVDVCSRLFDNDLPDGEWERRRTASGRIQVNLHIT 180
 DB 121 GENDNDTVRGQVWSLQSRDRIGTGQVVDVCSRLFDNDLPDGEWERRRTASGRIQVNLHIT 180

QY 181 RTTOWERPTRPASEYSSPGRLSCFVDENTPISGTNGATCGQSSDPRLAERVRVSQRHN 240
 DB 181 RTTOWERPTRPASEYSSPGRLSCFVDENTPISGTNGATCGQSSDPRLAERVRVSQRHN 240

QY 241 YMSRTHLHTPPDLPEGYEORTTQQGVYFLHTQTGTSTWHDPRVPRDLNSINCEELGFLP 300
 DB 241 YMSRTHLHTPPDLPEGYEORTTQQGVYFLHTQTGTSTWHDPRVPRDLNSINCEELGFLP 300

QY 301 PGWEIRNTATGRVYFVDHNNRTTQFTDPRLSANLHLVLRNQNLKDDQQQQVSLCPDPT 360
 DB 301 PGWEIRNTATGRVYFVDHNNRTTQFTDPRLSANLHLVLRNQNLKDDQQQQVSLCPDPT 360

QY 361 ECLTVPRYKRDVLQKILKRLQELSQOQOAGHCRIEVSREEIFEEYSYQVMKMRPKDLWK 420
 DB 361 ECLTVPRYKRDVLQKILKRLQELSQOQOAGHCRIEVSREEIFEEYSYQVMKMRPKDLWK 420

QY 421 RLMIKPRGEGLDYGVAREWLYLSHEMLNPPYGLFQYSRDDIYTLQINPDSAVNPEHL 480
 DB 421 RLMIKPRGEGLDYGVAREWLYLSHEMLNPPYGLFQYSRDDIYTLQINPDSAVNPEHL 480

QY 481 SYFHFVGRIMGMAVFGHYIDGGFTLPFYKQLLGKSIITLDDMLVDPLDLSLWILEND 540
 DB 481 SYFHFVGRIMGMAVFGHYIDGGFTLPFYKQLLGKSIITLDDMLVDPLDLSLWILEND 540

QY 541 ITGVLDHTFCVEHNAIGEIIQHELKPKNGKSIIPVNEENKKEYVRLYVNWFLRGIEAQFLA 600
 DB 541 ITGVLDHTFCVEHNAIGEIIQHELKPKNGKSIIPVNEENKKEYVRLYVNWFLRGIEAQFLA 600

QY 601 LQKGFNEVTPHLLKTFFDEKELELIICGLKIDVNDWKVNTLKHCTPDSNIVKWFKAV 660
 DB 601 LQKGFNEVTPHLLKTFFDEKELELIICGLKIDVNDWKVNTLKHCTPDSNIVKWFKAV 660

QY 661 EFFDEERRARLLQFVGTSSRPVLPQGFALQGAAGPRFLTTHQIDACTNLLPKAHTCFNRI 720
 DB 661 EFFDEERRARLLQFVGTSSRPVLPQGFALQGAAGPRFLTTHQIDACTNLLPKAHTCFNRI 720

QY 721 DIPPEYSYKLYEKLJTAIETCGFAVE 748
 DB 721 DIPPEYSYKLYEKLJTAIETCGFAVE 748

RESULT 2
 AAW13384
 ID AAW13384 standard; protein; 748 AA.
 XX
 AC AAW13384;
 XX
 PT 10-JUL-1997 (first entry)

XX DE Human protein ubiquitin ligase publi.
 XX KW Protein ubiquitin ligase; publi; cdc25 phosphatase; CDK kinase; p53;
 XX KW cell cycle; transgenic animal.
 XX OS Homo sapiens.
 XX PN WO9712962-AL.
 XX PD 10-APR-1997.
 XX PF 04-OCT-1996; 96WO-US015930.
 XX PR 04-OCT-1995; 95US-00539205.
 XX PA (COLD-) COLD SPRING HARBOR LAB.
 XX PI Beach D, Caligiuri M, Nefsky B;
 XX DR WPI; 1997-226206/20.
 XX XX N-PSDB; AAT47040.
 PT Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved in
 PT cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and
 PT proliferation.
 XX PS Claim 1; Page 74-77; 108pp; English.
 XX CC Human protein ubiquitin ligases publi (AAW13384), publi (AAW13385) and publi
 CC (AAW1386) are homologues of fission yeast publi (AAW13387) and were
 CC identified from cDNA clones (AAT47040-42) obt'd. e.g. from a keratinocyte
 CC cDNA library. Pub polypeptides can be produced in transfected host cells.
 CC They can control the steady state level of cdc25 phosphatase, the degree
 CC of CDK kinase (e.g. cdc2) dephosphorylation and the steady state level of
 CC p53 (controlling the degree of cell cycle regulation of p53). They can
 CC regulate cell or tissue differentiation, or cell growth or proliferation
 CC by affecting other proteins, can be a specific (ant)agonist of wild-type
 CC protein function and may be used as immunogens to elicit a specific
 CC immune residue

XX SQ Sequence 748 AA;

Query Match 99.8%; Score 4031; DB 2; Length 748;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 747; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPGRRNGPVKRLTLVLCANLVKDDFFRLPDPFAKVVVDGSGQCHSTDTVKNTLDPK 60
 DB 1 MSNPGRRNGPVKRLTLVLCANLVKDDFFRLPDPFAKVVVDGSGQCHSTDTVKNTLDPK 60

QY 61 WNOHYDLYIGKSDSVTISVWVNHKKIHKQAGFLGCVRLLSNAINRLKDTGYQRLDLCKL 120
 DB 61 WNOHYDLYIGKSDSVTISVWVNHKKIHKQAGFLGCVRLLSNAINRLKDTGYQRLDLCKL 120

QY 121 GENDNDTVRGQVWSLQSRDRIGTGQVVDVCSRLFDNDLPDGEWERRRTASGRIQVNLHIT 180
 DB 121 GENDNDTVRGQVWSLQSRDRIGTGQVVDVCSRLFDNDLPDGEWERRRTASGRIQVNLHIT 180

QY 181 RTTOWERPTRPASEYSSPGRLSCFVDENTPISGTNGATCGQSSDPRLAERVRVSQRHN 240
 DB 181 RTTOWERPTRPASEYSSPGRLSCFVDENTPISGTNGATCGQSSDPRLAERVRVSQRHN 240

QY 241 YMSRTHLHTPPDLPEGYEORTTQQGVYFLHTQTGTSTWHDPRVPRDLNSINCEELGFLP 300
 DB 241 YMSRTHLHTPPDLPEGYEORTTQQGVYFLHTQTGTSTWHDPRVPRDLNSINCEELGFLP 300

QY 301 PGWEIRNTATGRVYFVDHNNRTTQFTDPRLSANLHLVLRNQNLKDDQQQQVSLCPDPT 360
 DB 301 PGWEIRNTATGRVYFVDHNNRTTQFTDPRLSANLHLVLRNQNLKDDQQQQVSLCPDPT 360

QY 361 ECLTVPRYKRDVLQKILKRLQELSQOQOAGHCRIEVSREEIFEEYSYQVMKMRPKDLWK 420
 DB 361 ECLTVPRYKRDVLQKILKRLQELSQOQOAGHCRIEVSREEIFEEYSYQVMKMRPKDLWK 420

See ID NO:4

